WHAT IS CLAIMED IS:

1. A PD-L1 bicyclic peptide mimetic comprising a polypeptide that comprises at least three cysteine residues, separated by at least two loop sequences, and a molecular scaffold which forms covalent bonds with the cysteine residues of the polypeptide such that at least two polypeptide loops are formed on the molecular scaffold, wherein the PD-L1 bicyclic peptide mimetic comprises an amino acid sequence of:

$$X_1C_1LX_2X_3IFC_2X_4LRKGX_5C_3X_6X_7X_8X_9KX_{10}$$

or a modified derivative, or pharmaceutically acceptable salt, thereof;

wherein:

C_1, C_2, and C_3 represent first, second and third cysteine residues, respectively;

X_1 is absent or alanine;

X_2 is selected from any small amino acid (optionally, threonine, glycine, serine, or alanine, and preferably threonine or alanine, and most preferably, threonine);

X_3 is selected from any amino acid (preferably phenylalanine or alanine, and most preferably, phenylalanine);

X_4 is selected from any amino acid (preferably arginine or alanine, and most preferably, arginine);

X_5 is selected from any amino acid (preferably arginine or alanine, and most preferably, arginine);

X_6 is selected from any nonpolar/neutral amino acid (e.g., methionine, alanine, leucine, proline, glycine, isoleucine, phenylalanine, tryptophan, valine, or norleucine; preferably methionine, alanine, leucine, or proline; and most preferably, methionine);

X_7 is selected from any nonpolar/neutral amino acid (e.g., methionine, alanine, proline, leucine, glycine, isoleucine, phenylalanine, tryptophan, valine, or norleucine; preferably methionine, alanine or proline; and most preferably, methionine or alanine);

X_8 is selected from any amino acid (preferably, aspartic acid, alanine, glycine, or valine; and most preferably, aspartic acid);

X_9 is selected from any nonpolar/neutral amino acid (e.g., valine, alanine, glycine, methionine, leucine, proline, isoleucine, phenylalanine, tryptophan, or norleucine; preferably valine, alanine, glycine or methionine; and most preferably valine); and

X_{10} is selected from any amino acid (preferably lysine, alanine, asparagine, or methionine; and most preferably, lysine).

2. The PD-L1 bicyclic peptide mimetic of claim 1, wherein the peptide mimetic mimetic binds to importin, preferably preventing or disrupting the complex between PD-L1 and importin, preferably preventing or disrupting the complex between PD-L1 and importin.

3. The PD-L1 bicyclic peptide mimetic of claim 1 or claim 2, comprising the amino acid sequence: ACLTFIFCRLRKGRCMMDVKK [SEQ ID NO: 1].

4. The PD-L1 bicyclic peptide mimetic of any one of claims 1-3 , wherein the molecular scaffold is 1,3,5-(tribroMoMethyl)benzene) or TBAB.

5. The PD-L1 bicyclic peptide mimetic of any one of claims 1-4 , further comprising an N-terminal cell-penetrating peptide (for example, Myr).

6. The PD-L1 bicyclic peptide mimetic of any one of claims 1-5, wherein the modified derivative includes one or more modifications selected from: N-terminal and/or C-terminal modifications; replacement of one or more amino acid residues with one or more non-natural amino acid residues (such a replacement of one or more polar amino acids with one or more isosteric or isoelectronic amino acids; replacement or one or more hydrophobic amino acid residues with other non-natural isosteric or isoelectronic amino acids); addition of a spacer group; replacement of one or more oxidation resistant amino acid residues; replacement of one or more amino acid residues with an alanine, replacement of one or more L amino acid residues with one or more D-amino acid residues; N-alkylation of one or more aminide bonds within the bicyclic peptide ligand; replacement of one or more peptide bonds with a surrogate bond; peptide backbone length modification; substitution of the hydrogen on the α-carbon of one or more amino acid residues with another chemical group, and post-synthetic biorthogonal modification of amino acids such as cysteine, lysine, glutamate and tyrosine with suitable amine, thiol, carboxylic acid and phenol-reactive reagents.

7. The PD-L1 bicyclic peptide mimetic of any one of claims 1-6 , wherein the modified derivative comprises one or more D-amino acid (for example, wherein substantially all of the amino acids are D-amino acids).

8. The PD-L1 bicyclic peptide mimetic of any one of claims 1 to 7 , wherein the peptide is formulated in a lipid nanoparticle.

9. The PD-L1 bicyclic peptide mimetic of any one of claims 1-8 , wherein the pharmaceutically acceptable salt is selected from a hydrochloride or acetate salt.

10. A pharmaceutical composition comprising the PD-L1 bicyclic peptide mimetic of any one of claims 1-9, in combination with one or more excipients.

11. A method of reducing nuclear localization of PD-L1 in a PD-L1 overexpressing cell, the method comprising contacting the cell with a PD-L1 bicyclic peptide mimetic with the amino acid sequence of:

$$X_1C_1LX_2X_3IFC_2X_4LRKGX_5C_3X_6X_7X_8X_9KX_{10}$$

or a modified derivative, or pharmaceutically acceptable salt, thereof;

wherein:

C_1, C_2, and C_3 represent first, second and third cysteine residues, respectively;

X_1 is absent or alanine;

X_2 is selected from any small amino acid (optionally, threonine, glycine, serine, or alanine, and preferably threonine or alanine, and most preferably, threonine);

X_3 is selected from any amino acid (preferably phenylalanine or alanine, and most preferably, phenylalanine);

X_4 is selected from any amino acid (preferably arginine or alanine, and most preferably, arginine);

X_5 is selected from any amino acid (preferably arginine or alanine, and most preferably, arginine);

X_6 is selected from any nonpolar/neutral amino acid (e.g., methionine, alanine, leucine, proline, glycine, isoleucine, phenylalanine, tryptophan, valine, or norleucine, preferably methionine, alanine, leucine, or proline; and most preferably, methionine);

X_7 is selected from any nonpolar/neutral amino acid (e.g., methionine, alanine, proline, leucine, glycine, isoleucine, phenylalanine, tryptophan, valine, and norleucine, preferably methionine, alanine or proline, and most preferably, methionine or alanine);

X_8 is selected from any amino acid (preferably, aspartic acid, alanine, glycine, or valine, and most preferably, aspartic acid);

X_9 is selected from any nonpolar/neutral amino acid (e.g., valine, alanine, glycine, methionine, leucine, proline, isoleucine, phenylalanine, tryptophan, or norleucine, preferably valine, alanine, glycine or methionine; and most preferably valine); and

X_{10} is selected from any amino acid (preferably lysine, alanine, asparagine, or methionine, and most preferably, lysine).

12. The method of claim 11, comprising the amino acid sequence: ACLTFIFCRLRKGRCMMDVKK [SEQ ID NO: 1].

13. The method of claim 11 or claim 12, wherein the molecular scaffold is 1,3,5-(tribroMoMethyl)benzene) or TBAB.

14. The method of any one of claims 11 to 13 , wherein the modified derivative comprises one or more D-amino acid (for example, all of the amino acids are D-amino acids) (for example, all of the amino acids are D-amino acids).

15. The method of any one of claims 11 to 14 , wherein the peptide is formulated in a lipid nanoparticle.

16. The method of any one of claims 11 to 15 , further comprising an N-terminal cell-penetrating peptide (for example, myristic acid).

17. A method of treating or preventing cancer in a subject, wherein the cancer comprises at least one PD-L1 overexpressing cell, comprising administering to the subject a PD-L1 bicyclic peptide mimetic of any one of claims 1 to 10.

18. The method of any one of claims 11 to 17 , wherein the PD-L1 overexpressing cell is a cancer cell, cancer stem cell, or a non-cancer stem cell tumour cell.

19. The method of any one of claims11 to 18, wherein the cancer is selected from breast, prostate, lung, bladder, pancreatic, colon, liver, or brain cancer, or melanoma, or retinoblastoma.

20. The method of any one of claims 11 to 19 , further comprising administering at least one further cancer therapies (e.g., a chemotherapeutic agent).